

SEQUENCE LISTING

<110> Universiteit Utrecht Holding B.V.

<120> Piroplasmid vaccine

<130> 2003-010

<160> 20

<170> PatentIn version 3.2

<210> 1

<211> 1818

<212> DNA

<213> Babesia bovis

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Phe Ala Glu Asp Ala Leu Ala Ser Asn Ser Thr Leu Phe Ala Phe His	
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Arg Tyr Pro Gly Arg Ser Gly Ser Lys Asn Ser Ser Gln Ser Pro	
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tgg atc aag tat atg caa aag ttc gac att ccc cgt aac cac ggc tct	336
Trp Ile Lys Tyr Met Gln Lys Phe Asp Ile Pro Arg Asn His Gly Ser	
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gga atc tat gtc gat ctt gga gga tat gaa tcc gtt ggt tca aaa agt	384
Gly Ile Tyr Val Asp Leu Gly Gly Tyr Glu Ser Val Gly Ser Lys Ser	
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Tyr Arg Met Pro Val Gly Lys Cys Pro Val Val Gly Lys Ile Ile Asp	
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aac cag atg tgt tac ata ctg tac tct gcc ata caa tac aac caa gga Asn Gln Met Cys Tyr Ile Leu Tyr Ser Ala Ile Gln Tyr Asn Gln Gly				768
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275		280		285
tac ggt tct gcg aaa gtt gac ccc gat tgg gaa gaa aat tgt ccc atg Tyr Gly Ser Ala Lys Val Asp Pro Asp Trp Glu Asn Cys Pro Met				912
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				400

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Lys Glu Pro Asn Asn Arg Arg Leu Thr Lys Arg Ser Ser Arg Gly Gln
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Leu Leu Asn Ser Arg Arg Gly Ser Asp Asp Ala Ser Glu Ser Ser Asp
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Gly Ile Tyr Val Asp Leu Gly Gly Tyr Glu Ser Val Gly Ser Lys Ser
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Ser Tyr Arg Gly Leu Ala Phe Pro Glu Thr Ala Val Asp Ser Asn Ile
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Leu Ser Pro Val Ser Ala Lys Asp Leu Arg Arg Trp Gly Tyr Glu Gly
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Leu Leu Cys Met Lys Pro Tyr Lys Ser Ala Glu Asp Ala His Leu Tyr
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His Pro Val Arg Asp Ala Ile Phe Gly Lys Trp Ser Gly Gly Ser Cys
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Val Ala Ile Ala Pro Ala Phe Gln Glu Tyr Ala Asn Ser Thr Glu Asp
325 330 335

Cys Ala Ala Ile Leu Phe Asp Asn Ser Ala Thr Asp Leu Asn Ile Glu
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Ser Asn Val Ala Gly Thr Ser Arg Ile Ser Arg Gly Val Gly Met Asn
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490

495

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 Gln Gln Asn Val Phe Thr His Gln Pro Thr Gln Leu His Lys Ser His
 35 40 45

cac tac att aca cac cag aaa aaa acc agc caa cac atc gac gat tta 192
 His Tyr Ile Thr His Gln Lys Lys Thr Ser Gln His Ile Asp Asp Leu
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att tta cct aga ctt tta aaa tct tta tca ttt tta gct gtt tta ggg Ile Leu Pro Arg Leu Leu Lys Ser Leu Ser Phe Leu Ala Val Leu Gly 115 120 125				384
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agg aat aac gta tta aac aga aca cta ggt aga ttc gga tca ttt ttg Arg Asn Asn Val Leu Asn Arg Thr Leu Gly Arg Phe Gly Ser Phe Leu 195 200 205				624
caa tca gga ttg ata agc agt aga gca gac aaa aag aag cgg tct ggt Gln Ser Gly Leu Ile Ser Ser Arg Ala Asp Lys Lys Lys Arg Ser Gly 210 215 220				672
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gct tgt atg tac ccg gat aag agc aag gag gat tca cac cta ttt tac Ala Cys Met Tyr Pro Asp Lys Ser Lys Glu Asp Ser His Leu Phe Tyr 420 425 430	1296
gga acc agc ggt ctt cac atg gac tgg cct gta gtt tgc cca gtt tac Gly Thr Ser Gly Leu His Met Asp Trp Pro Val Val Cys Pro Val Tyr 435 440 445	1344
cct att aga gat tcg att ttt gga tcc tac gac gac caa aag gac gaa Pro Ile Arg Asp Ser Ile Phe Gly Ser Tyr Asp Asp Gln Lys Asp Glu 450 455 460	1392
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cac ttg aaa aaa cac aat tcc cag ata tat gaa gat gat aac gtg aac His Leu Lys His Asn Ser Gln Ile Tyr Glu Asp Asp Asn Val Asn 725 730 735	2208
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His Tyr Ile Thr His Gln Lys Lys Thr Ser Gln His Ile Asp Asp Leu
50 55 60

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85 90 95

Lys Asp Asp Asn Lys Thr Lys Ser Lys Ile Lys Ser Lys Thr Ala Ser
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Ile Leu Pro Arg Leu Leu Lys Ser Leu Ser Phe Leu Ala Val Leu Gly
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Ser Ile Asn Ser Phe Ser Leu Ala Leu Glu Glu Pro Phe Thr Gln His
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Thr Ser Asn Arg Thr Pro Phe Glu Val Ser Leu Ile Gln Ser Asn Ser
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Ser Leu Ser Pro Ile His Asn Ser Ser Thr Gln Asn Ser Ser His His
165 170 175

Asn Gly Phe Ser Gly Ser Thr Val Asn Asn Thr Ser Leu Ile Glu Thr
180 185 190

Arg Asn Asn Val Leu Asn Arg Thr Leu Gly Arg Phe Gly Ser Phe Leu
195 200 205

Gln Ser Gly Leu Ile Ser Ser Arg Ala Asp Lys Lys Lys Arg Ser Gly
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565 570 575

Leu Ser Ser Pro Asn Glu Glu Asp Ala Ile Asn Tyr Pro Cys Asp Ile
580 585 590

Val Gln Gly Lys Gly Phe Leu Lys Asn Pro Asn Gly Gly Lys Lys Asn
595 600 605

Ala Gln Glu Pro Pro Lys Glu Pro Glu Pro Glu Glu Pro Lys Lys Glu
610 615 620

Gly Ala Glu Asn Lys Pro Lys Glu Lys Gly Lys Ser Glu Lys Lys Asn
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Glu Lys Ser Met Pro Ser Gly Pro Phe Thr Pro Tyr Thr Ser Leu Lys
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Ser Cys Gly Val Tyr Tyr Glu Cys Ser Glu Thr Pro Val Leu Phe Thr
675 680 685

Lys Lys Asn Arg Ile Tyr Leu Tyr Ile Ile Leu Ala Val Ser Leu Val
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Val Leu Ala Val Leu Ala Tyr Phe Gly Tyr Arg Tyr Tyr Ser Lys Asn
705 710 715 720

His Leu Lys Lys His Asn Ser Gln Ile Tyr Glu Asp Asp Asn Val Asn
 725 730 735

Asn Tyr Tyr Asn Glu Asp Phe Asp Asp Glu Gln Asp Arg Asp Glu Tyr
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Gly Ser Pro Lys Gly Lys Gln Cys Lys Lys Gln Leu Asp Phe Ser Ile	
35 40 45	
gtg gta gat gaa tct gct agt ata tcg gat gat caa tgg gag ggt cag	192
Val Val Asp Glu Ser Ala Ser Ile Ser Asp Asp Gln Trp Glu Gly Gln	
50 55 60	
atg att cca ttt ttg agg aat ttg att cat acc gtt gac ctt gac aac	240
Met Ile Pro Phe Leu Arg Asn Leu Ile His Thr Val Asp Leu Asp Asn	
65 70 75 80	
act gac ata cgt ctt tcg ctt acc act tac tca act cca act cgc cag	288
Thr Asp Ile Arg Leu Ser Leu Thr Thr Tyr Ser Thr Pro Thr Arg Gln	
85 90 95	
ata ttt acg ttt ttg gat gct gct gca agc agt acc agg ctc gca ctc	336
Ile Phe Thr Phe Leu Asp Ala Ala Ser Ser Thr Arg Leu Ala Leu	
100 105 110	
acg aaa ctt gat tgg atg aac ggt acc aaa gct agg tat ggt atg acc	384
Thr Lys Leu Asp Trp Met Asn Gly Thr Lys Ala Arg Tyr Gly Met Thr	
115 120 125	

tac act ggc agg gct ctg aac tac gtt cgt aag gct ata cta cca tat Tyr Thr Gly Arg Ala Leu Asn Tyr Val Arg Lys Ala Ile Leu Pro Tyr 130 135 140	432
ggt cgc aag aat gta ccc aag gca ctg tta ctg atc act gat gga gta Gly Arg Lys Asn Val Pro Lys Ala Leu Leu Ile Thr Asp Gly Val 145 150 155 160	480
tct tcg gat gga agt tac act gca cag gtt gcg gct atg ctt cgt gat Ser Ser Asp Gly Ser Tyr Thr Ala Gln Val Ala Ala Met Leu Arg Asp 165 170 175	528
gaa ggt gta aat gta atg gtt att ggt gtc ggt gat gta aat gtt gct Glu Gly Val Asn Val Met Val Ile Gly Val Gly Asp Val Asn Val Ala 180 185 190	576
gaa tgc cgt ggc ata gta gga tgt gat gga ata atg gat tgt cct atg Glu Cys Arg Gly Ile Val Gly Cys Asp Gly Ile Met Asp Cys Pro Met 195 200 205	624
ttc aag cag acc aac tgg aag gat atc atg ggc ctc ttt aac agt tta Phe Lys Gln Thr Asn Trp Lys Asp Ile Met Gly Leu Phe Asn Ser Ile 210 215 220	672
atg aag gag gta tgt gat att tta cct cag gac gct gtt tgt gag cct Met Lys Glu Val Cys Asp Ile Leu Pro Gln Asp Ala Val Cys Glu Pro 225 230 235 240	720
gta tgg gca gaa tgg tca tct tgt aac ggg gaa tgt ggc gtt cct ggt Val Trp Ala Glu Trp Ser Ser Cys Asn Gly Glu Cys Gly Val Pro Gly 245 250 255	768
aaa cga act cgt gct ctt ttg gac ctc cga atg att gaa aag ccc gta Lys Arg Thr Arg Ala Leu Leu Asp Leu Arg Met Ile Glu Lys Pro Val 260 265 270	816
aat ggc tcg aat gga caa ccg ggt aaa tca tgt gag gat cag aag atg Asn Gly Ser Asn Gly Gln Pro Gly Lys Ser Cys Glu Asp Gln Lys Met 275 280 285	864
aac ttc tta ccc caa tca gag aca tgc acc ata gaa tgc aat cat gag Asn Phe Leu Pro Gln Ser Glu Thr Cys Thr Ile Glu Cys Asn His Glu 290 295 300	912
cct gtg cca agc tcg ccg gaa cct gta tca gat gat atg gat cac cca Pro Val Pro Ser Ser Pro Glu Pro Val Ser Asp Asp Met Asp His Pro 305 310 315 320	960
gaa cca act cct gtt aca ccg gaa ggt gac atg gat aaa tct cat tcc Glu Pro Thr Pro Val Thr Pro Glu Gly Asp Met Asp Lys Ser His Ser 325 330 335	1008
cat tcg agc att cca tcc acc cct gat atg cca tca agt cac agt gat His Ser Ser Ile Pro Ser Thr Pro Asp Met Pro Ser Ser His Ser Asp 340 345 350	1056
atg tca tca agc cct act gat atg tca tca agc cct act gac atg tca Met Ser Ser Pro Thr Asp Met Ser Ser Ser Pro Thr Asp Met Ser 355 360 365	1104
tca agc cct act gac atg tca tca agt cac agt gac atg cca tca act	1152

Ser Ser Pro Thr Asp Met Ser Ser Ser His Ser Asp Met Pro Ser Thr			
370	375	380	
cct act ggc atg tca tca agt cac agt gat atg cca tca agt cac agt			1200
Pro Thr Gly Met Ser Ser Ser His Ser Asp Met Pro Ser Ser His Ser			
385	390	395	400
gat atg cca tca agc cac agt gat atg tca tca agc cct act gac atg			1248
Asp Met Pro Ser Ser His Ser Asp Met Ser Ser Ser Pro Thr Asp Met			
405	410	415	
tca tca agt cac gct gat act cgt gta gga aat acc gat gaa gaa cat			1296
Ser Ser Ser His Ala Asp Thr Arg Val Gly Asn Thr Asp Glu Glu His			
420	425	430	
aac cac agg aaa gat atg gat gtc aag ttc ccc gaa aat atg gat gat			1344
Asn His Arg Lys Asp Met Asp Val Lys Phe Pro Glu Asn Met Asp Asp			
435	440	445	
atc cca gtc gag gat aat cct ata ccc aca gat cct aga cat ggc gtc			1392
Ile Pro Val Glu Asp Asn Pro Ile Pro Thr Asp Pro Arg His Gly Val			
450	455	460	
gaa cca tcg cct tct gat gtg atc cct gag gat gac caa ctt cgt agg			1440
Glu Pro Ser Pro Asp Val Ile Pro Glu Asp Asp Gln Leu Arg Arg			
465	470	475	480
acg ctt gaa atg cag cgc gaa gag gac cta aag aag gaa ttg atg ctc			1488
Thr Leu Glu Met Gln Arg Glu Glu Asp Leu Lys Lys Glu Leu Met Leu			
485	490	495	
caa cat gaa ctg aag ctt cag gaa gaa aag gaa agg gca gct att tta			1536
Gln His Glu Leu Lys Leu Gln Glu Lys Glu Arg Ala Ala Ile Leu			
500	505	510	
gag aat aac act cct tat gga tcc gcc act tcc gtg tcg caa gac ggt			1584
Glu Asn Asn Thr Pro Tyr Gly Ser Ala Thr Ser Val Ser Gln Asp Gly			
515	520	525	
gaa tct cca act ggc gta ccc caa agt agc gag acc gat gca ata cgt			1632
Glu Ser Pro Thr Gly Val Pro Gln Ser Ser Glu Thr Asp Ala Ile Arg			
530	535	540	
cac gag gtg tat gac gat cac ccc gag gaa tct gaa aac acc ggg att			1680
His Glu Val Tyr Asp Asp His Pro Glu Glu Ser Glu Asn Thr Gly Ile			
545	550	555	560
aat gct gat gtg acc gaa tct gag gac tat gag ggt gaa aaa caa aag			1728
Asn Ala Asp Val Thr Glu Ser Glu Asp Tyr Glu Gly Glu Lys Gln Lys			
565	570	575	
gac gaa tca aat gaa cgt tcg acc agc aac act act aag att gcc ggc			1776
Asp Glu Ser Asn Glu Arg Ser Thr Ser Asn Thr Thr Lys Ile Ala Gly			
580	585	590	
ggt gct cta cta ggt ctt ctt ctc ctt ggt gcc ggt ggt gga tac gct			1824
Gly Ala Leu Leu Gly Leu Leu Leu Leu Gly Ala Gly Gly Tyr Ala			
595	600	605	
atg tac aaa aag aac aag aca cct act gtt gag aca ggt tca ggt gat			1872
Met Tyr Lys Lys Asn Lys Thr Pro Thr Val Glu Thr Gly Ser Gly Asp			

610	615	620	
tac act ggg gcc gac gag agt tca gaa ccc atg aag gag ggt gac aca Tyr Thr Gly Ala Asp Glu Ser Ser Glu Pro Met Lys Glu Gly Asp Thr 625	630	635	1920
tac acc gtc act gag ttt gac aac aac att tgg ggc gag gca gcg taa Tyr Thr Val Thr Glu Phe Asp Asn Asn Ile Trp Gly Glu Ala Ala 645	650	655	1968
<210> 6			
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<213> Babesia bovis			
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Ala Phe Leu Ala Thr Thr Gly Ile His Ala Phe Ala Asp Lys Gly Ile 20 25 30			
Gly Ser Pro Lys Gly Lys Gln Cys Lys Lys Gln Leu Asp Phe Ser Ile 35 40 45			
Val Val Asp Glu Ser Ala Ser Ile Ser Asp Asp Gln Trp Glu Gly Gln 50 55 60			
Met Ile Pro Phe Leu Arg Asn Leu Ile His Thr Val Asp Leu Asp Asn 65 70 75 80			
Thr Asp Ile Arg Leu Ser Leu Thr Thr Tyr Ser Thr Pro Thr Arg Gln 85 90 95			
Ile Phe Thr Phe Leu Asp Ala Ala Ala Ser Ser Thr Arg Leu Ala Leu 100 105 110			
Thr Lys Leu Asp Trp Met Asn Gly Thr Lys Ala Arg Tyr Gly Met Thr 115 120 125			
Tyr Thr Gly Arg Ala Leu Asn Tyr Val Arg Lys Ala Ile Leu Pro Tyr 130 135 140			
Gly Arg Lys Asn Val Pro Lys Ala Leu Leu Ile Thr Asp Gly Val 145 150 155 160			
Ser Ser Asp Gly Ser Tyr Thr Ala Gln Val Ala Ala Met Leu Arg Asp 165 170 175			

Glu Gly Val Asn Val Met Val Ile Gly Val Gly Asp Val Asn Val Ala
180 185 190

Glu Cys Arg Gly Ile Val Gly Cys Asp Gly Ile Met Asp Cys Pro Met
195 200 205

Phe Lys Gln Thr Asn Trp Lys Asp Ile Met Gly Leu Phe Asn Ser Leu
210 215 220

Met Lys Glu Val Cys Asp Ile Leu Pro Gln Asp Ala Val Cys Glu Pro
225 230 235 240

Val Trp Ala Glu Trp Ser Ser Cys Asn Gly Glu Cys Gly Val Pro Gly
245 250 255

Lys Arg Thr Arg Ala Leu Leu Asp Leu Arg Met Ile Glu Lys Pro Val
260 265 270

Asn Gly Ser Asn Gly Gln Pro Gly Lys Ser Cys Glu Asp Gln Lys Met
275 280 285

Asn Phe Leu Pro Gln Ser Glu Thr Cys Thr Ile Glu Cys Asn His Glu
290 295 300

Pro Val Pro Ser Ser Pro Glu Pro Val Ser Asp Asp Met Asp His Pro
305 310 315 320

Glu Pro Thr Pro Val Thr Pro Glu Gly Asp Met Asp Lys Ser His Ser
325 330 335

His Ser Ser Ile Pro Ser Thr Pro Asp Met Pro Ser Ser His Ser Asp
340 345 350

Met Ser Ser Ser Pro Thr Asp Met Ser Ser Ser Pro Thr Asp Met Ser
355 360 365

Ser Ser Pro Thr Asp Met Ser Ser Ser His Ser Asp Met Pro Ser Thr
370 375 380

Pro Thr Gly Met Ser Ser Ser His Ser Asp Met Pro Ser Ser His Ser
385 390 395 400

Asp Met Pro Ser Ser His Ser Asp Met Ser Ser Ser Pro Thr Asp Met
405 410 415

Ser Ser Ser His Ala Asp Thr Arg Val Gly Asn Thr Asp Glu Glu His
420 425 430

Asn His Arg Lys Asp Met Asp Val Lys Phe Pro Glu Asn Met Asp Asp
435 440 445

Ile Pro Val Glu Asp Asn Pro Ile Pro Thr Asp Pro Arg His Gly Val
450 455 460

Glu Pro Ser Pro Ser Asp Val Ile Pro Glu Asp Asp Gln Leu Arg Arg
465 470 475 480

Thr Leu Glu Met Gln Arg Glu Glu Asp Leu Lys Lys Glu Leu Met Leu
485 490 495

Gln His Glu Leu Lys Leu Gln Glu Glu Lys Glu Arg Ala Ala Ile Leu
500 505 510

Glu Asn Asn Thr Pro Tyr Gly Ser Ala Thr Ser Val Ser Gln Asp Gly
515 520 525

Glu Ser Pro Thr Gly Val Pro Gln Ser Ser Glu Thr Asp Ala Ile Arg
530 535 540

His Glu Val Tyr Asp Asp His Pro Glu Glu Ser Glu Asn Thr Gly Ile
545 550 555 560

Asn Ala Asp Val Thr Glu Ser Glu Asp Tyr Glu Gly Glu Lys Gln Lys
565 570 575

Asp Glu Ser Asn Glu Arg Ser Thr Ser Asn Thr Thr Lys Ile Ala Gly
580 585 590

Gly Ala Leu Leu Gly Leu Leu Leu Leu Gly Ala Gly Gly Tyr Ala
595 600 605

Met Tyr Lys Lys Asn Lys Thr Pro Thr Val Glu Thr Gly Ser Gly Asp
610 615 620

Tyr Thr Gly Ala Asp Glu Ser Ser Glu Pro Met Lys Glu Gly Asp Thr
625 630 635 640

Tyr Thr Val Thr Glu Phe Asp Asn Asn Ile Trp Gly Glu Ala Ala
645 650 655

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<211> 1047
<212> DNA
<213> Theileria annulata

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Asp Lys Gly Leu Tyr Pro Asp Gly Ile Lys Lys Pro Ser Ser Tyr Cys
1           5           10          15

cac agg gaa ttg gac tta aca ata tta gtc gat gaa tcc tcg agt atc      96
His Arg Glu Leu Asp Leu Thr Ile Leu Val Asp Glu Ser Ser Ser Ile
20          25          30

tat att gaa gag tgg aac aaa ctc att cca ttt ctt aaa tca ctg gtg      144
Tyr Ile Glu Glu Trp Asn Lys Leu Ile Pro Phe Leu Lys Ser Leu Val
35          40          45

aga tca ata aat ata agt cca aat tat gtg cac ttg tca atg gtc acc      192
Arg Ser Ile Asn Ile Ser Pro Asn Tyr Val His Leu Ser Met Val Thr
50          55          60

ttt tcc act tca att cgg tgg tta ata tca ttt ctc gac cca gcc tct      240
Phe Ser Thr Ser Ile Arg Trp Leu Ile Ser Phe Leu Asp Pro Ala Ser
65          70          75          80

aag gat gag caa ttg gcc ctt gct gtt ctg gac aag ctg aag aac agt      288
Lys Asp Glu Gln Leu Ala Leu Ala Val Leu Asp Lys Leu Lys Asn Ser
85          90          95

aag cct gtg ttt ggg tac aca ttc act gga cag gca ctt aac ttt att      336
Lys Pro Val Phe Gly Tyr Thr Phe Thr Gly Gln Ala Leu Asn Phe Ile
100         105         110

tct gag gct tat atg ttt ggt gct agg cgt aac tct cca aag ggc      384
Ser Glu Ala Val Tyr Met Phe Gly Ala Arg Arg Asn Ser Pro Lys Gly
115         120         125

atc att atc atc acc gac gga tcc tct act cag aca aac gtt act tct      432
Ile Ile Ile Ile Thr Asp Gly Ser Ser Thr Gln Thr Asn Val Thr Ser
130         135         140

cag gcg tcg gct cta cta agg gat gct ggt gta aca att cta gtt gtt      480
Gln Ala Ser Ala Leu Leu Arg Asp Ala Gly Val Thr Ile Leu Val Val
145         150         155         160

gga gtt ggg aag gct aaa gaa agc gag tgt aga ggt ata gtt ggt tgt      528
Gly Val Gly Lys Ala Lys Glu Ser Glu Cys Arg Gly Ile Val Gly Cys
165         170         175

tct acc aaa gga gag tgc ccc ctt ttc ttt atg acc aac tgg gat gaa      576
Ser Thr Lys Gly Glu Cys Pro Leu Phe Phe Met Thr Asn Trp Asp Glu
180         185         190

att atc agg aag gtt ggg gag ttg atg gct gag gtt tgt gag acc att      624
Ile Ile Arg Lys Val Gly Glu Leu Met Ala Glu Val Cys Glu Thr Ile

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195	200	205	
cct aag gac gcc gta tgt aag ccg atc tgg tct gat tgg tct aag tgt Pro Lys Asp Ala Val Cys Lys Pro Ile Trp Ser Asp Trp Ser Lys Cys			672
210	215	220	
gac gcc aag tgc ggc att ggg acg agg tac caa aag ttg atg gga gtt Asp Ala Lys Cys Gly Ile Gly Thr Arg Tyr Gln Lys Leu Met Gly Val			720
225	230	235	240
act aca att tct gag cca act gtc gga acg aac ggc aag tcc ggg agg Thr Thr Ile Ser Glu Pro Thr Val Gly Thr Asn Gly Lys Ser Gly Arg			768
245	250	255	
aca tgt gag atg att tat gag aac gtc gag gtt cca aag gag gag tgc Thr Cys Glu Met Ile Tyr Glu Asn Val Glu Val Pro Lys Glu Glu Cys			816
260	265	270	
tcc gtt gag tct aag att gct gga gga gtg gct cta gca ctg tta atg Ser Val Glu Ser Lys Ile Ala Gly Gly Val Ala Leu Ala Leu Leu Met			864
275	280	285	
ctt gca ggc gga ggt ggt tac aca tac tac aaa aag tac ggt tta tct Leu Ala Gly Gly Gly Tyr Thr Tyr Tyr Lys Lys Tyr Gly Leu Ser			912
290	295	300	
aga gtg agt gaa act acg aat ttg gat gag gat ttt gca gat tct agt Arg Val Ser Glu Thr Thr Asn Leu Asp Glu Asp Phe Ala Asp Ser Ser			960
305	310	315	320
ggg aac cgt ggt gta agg gag agt gtg ggt gaa gct tac aca gta act Gly Asn Arg Gly Val Arg Glu Ser Val Gly Glu Ala Tyr Thr Val Thr			1008
325	330	335	
gat tta gat gat gga ctc tgg agc caa tcc aat caa taa Asp Leu Asp Asp Gly Leu Trp Ser Gln Ser Asn Gln			1047
340	345		
<210> 8			
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1	5	10	15
His Arg Glu Leu Asp Leu Thr Ile Leu Val Asp Glu Ser Ser Ser Ile			
20	25	30	
Tyr Ile Glu Glu Trp Asn Lys Leu Ile Pro Phe Leu Lys Ser Leu Val			
35	40	45	
Arg Ser Ile Asn Ile Ser Pro Asn Tyr Val His Leu Ser Met Val Thr			
50	55	60	

Phe Ser Thr Ser Ile Arg Trp Leu Ile Ser Phe Leu Asp Pro Ala Ser
65 70 75 80

Lys Asp Glu Gln Leu Ala Leu Ala Val Leu Asp Lys Leu Lys Asn Ser
85 90 95

Lys Pro Val Phe Gly Tyr Thr Phe Thr Gly Gln Ala Leu Asn Phe Ile
100 105 110

Ser Glu Ala Val Tyr Met Phe Gly Ala Arg Arg Asn Ser Pro Lys Gly
115 120 125

Ile Ile Ile Ile Thr Asp Gly Ser Ser Thr Gln Thr Asn Val Thr Ser
130 135 140

Gln Ala Ser Ala Leu Leu Arg Asp Ala Gly Val Thr Ile Leu Val Val
145 150 155 160

Gly Val Gly Lys Ala Lys Glu Ser Glu Cys Arg Gly Ile Val Gly Cys
165 170 175

Ser Thr Lys Gly Glu Cys Pro Leu Phe Phe Met Thr Asn Trp Asp Glu
180 185 190

Ile Ile Arg Lys Val Gly Glu Leu Met Ala Glu Val Cys Glu Thr Ile
195 200 205

Pro Lys Asp Ala Val Cys Lys Pro Ile Trp Ser Asp Trp Ser Lys Cys
210 215 220

Asp Ala Lys Cys Gly Ile Gly Thr Arg Tyr Gln Lys Leu Met Gly Val
225 230 235 240

Thr Thr Ile Ser Glu Pro Thr Val Gly Thr Asn Gly Lys Ser Gly Arg
245 250 255

Thr Cys Glu Met Ile Tyr Glu Asn Val Glu Val Pro Lys Glu Glu Cys
260 265 270

Ser Val Glu Ser Lys Ile Ala Gly Gly Val Ala Leu Ala Leu Leu Met
275 280 285

Leu Ala Gly Gly Gly Tyr Thr Tyr Tyr Lys Lys Tyr Gly Leu Ser
290 295 300

22/29

Arg Val Ser Glu Thr Thr Asn Leu Asp Glu Asp Phe Ala Asp Ser Ser
 305 310 315 320

Gly Asn Arg Gly Val Arg Glu Ser Val Gly Glu Ala Tyr Thr Val Thr
325 330 335

Asp Leu Asp Asp Gly Leu Trp Ser Gln Ser Asn Gln
340 345

<210> 9
<211> 2259
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<213> Babesia bovis

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tta aaa aaa tat gaa gga ata aat gtt tca cta ata agg tac aat agt Leu Lys Lys Tyr Glu Gly Ile Asn Val Ser Leu Ile Arg Tyr Asn Ser 95 100 105	878
gaa gaa ccg tta ggt tcg acg aaa gca tta acc aac ggg gag ttg aaa Glu Glu Pro Leu Gly Ser Thr Lys Ala Leu Thr Asn Gly Glu Leu Lys 110 115 120 125	926
aaa cta tcc gat aat att cct act aaa atg cct ttt gac att ggc gtt Lys Leu Ser Asp Asn Ile Pro Thr Lys Met Pro Phe Asp Ile Gly Val 130 135 140	974
gtt cct act ggt ata gga gct gcc ctc aaa cag ata aaa aca ttg tac Val Pro Thr Gly Ile Gly Ala Ala Leu Lys Gln Ile Lys Thr Leu Tyr 145 150 155	1022
cct gat cac gaa aag ttc ctt gtt ggg aac acc att act gag ttg gat Pro Asp His Glu Lys Phe Leu Val Gly Asn Thr Ile Thr Glu Leu Asp 160 165 170	1070
tat tct aaa gca ttg ggt aag gat att gtt gta atc gtg ttt act act Tyr Ser Lys Ala Leu Gly Lys Asp Ile Val Val Ile Val Phe Thr Thr 175 180 185	1118
ggc cac gtc att gat cca tat tta gca tat gat gag gca ttt gat gcc Gly His Val Ile Asp Pro Tyr Leu Ala Tyr Asp Glu Ala Phe Asp Ala 190 195 200 205	1166
cgc cgt aat ggt gta aga ttt tac gtt att aat agg gga gga aag gca Arg Arg Asn Gly Val Arg Phe Tyr Val Ile Asn Arg Gly Lys Ala 210 215 220	1214
aaa aac tat tgg act cag cta ttg gga tgc cac tac aat act tgt ttg Lys Asn Tyr Trp Thr Gln Leu Leu Gly Cys His Tyr Asn Thr Cys Leu 225 230 235	1262
agt tat att cgg gcc aaa ata aca agg cct tca cta tat ctc gat gtt Ser Tyr Ile Arg Ala Lys Ile Thr Arg Pro Ser Leu Tyr Leu Asp Val 240 245 250	1310
ttg gtg aac agg att gtg tct aaa cgc gcg aaa gat gcc gtt tgt ttg Leu Val Asn Arg Ile Val Ser Lys Arg Ala Lys Asp Ala Val Cys Leu 255 260 265	1358
gaa gtg tgg acg gat tat aaa cct aac act gaa aaa tcg gat gtg agg Glu Val Trp Thr Asp Tyr Lys Pro Asn Thr Glu Lys Ser Asp Val Arg 270 275 280 285	1406
att atg act tct acg ttg aaa tta tac aaa acc ctt ctt act gga agc Ile Met Thr Ser Thr Leu Lys Leu Tyr Lys Thr Leu Leu Thr Gly Ser 290 295 300	1454
ttt gcg gag ara aac atc aaa ggt ctc aca tgt gat gag cag cta aag Phe Ala Glu Xaa Asn Ile Lys Gly Leu Thr Cys Asp Glu Gln Leu Lys 305 310 315	1502
gat atg cag aaa aga caa ata ttt tgc tac tca aat aag tgt gct ccc	1550

Asp Met Gln Lys Arg Gln Ile Phe Cys Tyr Ser Asn Lys Cys Ala Pro		
320	325	330
acg atc tat tca aga tct tat gtt gac tta gct att caa cgt ctt aat		1598
Thr Ile Tyr Ser Arg Ser Tyr Val Asp Leu Ala Ile Gln Arg Leu Asn		
335	340	345
gca aaa gat ttt aaa gag gta cta gat gag tca tct tac aga tca cgc		1646
Ala Lys Asp Phe Lys Glu Val Leu Asp Glu Ser Ser Tyr Arg Ser Arg		
350	355	360
365		
agt ttg caa tca gtg gag aaa cat aat gag caa caa aca ggt tct caa		1694
Ser Leu Gln Ser Val Glu Lys His Asn Glu Gln Gln Thr Gly Ser Gln		
370	375	380
gaa acg ctt tct gga agc gcc cgt gta gaa aca agc tta gaa agc tca		1742
Glu Thr Leu Ser Gly Ser Ala Arg Val Glu Thr Ser Leu Glu Ser Ser		
385	390	395
400		
405		410
gta cct tca tcc tat gtg gca gaa ttg gga gaa agt gat aca gaa aca		1790
Val Pro Ser Ser Tyr Val Ala Glu Leu Gly Glu Ser Asp Thr Glu Thr		
415	420	425
tac aaa cag ttg gag tac ata gat aaa aat ggc gtc act gtc ttc aac		1838
Tyr Lys Gln Leu Glu Tyr Ile Asp Lys Asn Gly Val Thr Val Phe Asn		
425		
430		435
440		445
cat gaa aga gaa atg cag ttt gat gaa gaa tcc acc cat ctt ccc aac		1886
His Glu Arg Glu Met Gln Phe Asp Glu Glu Ser Thr His Leu Pro Asn		
450	455	460
465		
470		475
tct ggt aac cac cat cca cct cat cac cga aag ggg gcc aac gga tcc		1982
Ser Gly Asn His His Pro Pro His His Arg Lys Gly Ala Asn Gly Ser		
480	485	490
495		
500		505
510		
515		520
525		
gtg gaa ctc acc tct gaa gag ggt gac ttc ttg aac gac act acg ggt		2126
Val Glu Leu Thr Ser Glu Glu Gly Asp Phe Leu Asn Asp Thr Thr Gly		
530	535	540
545		
aaa aca tgg ttg taa gacacgaaac gggttgtcac agccaacata tacaaatgca		2174
Lys Thr Trp Leu		
545		
gtttaaatta agtcactagt taaaaaaaaaa		2229
		2259

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<222> (305)..(305)
<223> The 'Xaa' at location 305 stands for Arg, or Lys.

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Met Val Lys Phe His Thr Leu Ser Val Ala Ala Ile Leu Ala Ile Ala
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20 25 30

Gly Asp Glu Ser Val Ser Leu Leu Glu His Glu Ser Thr Ser Leu Ser
35 40 45

Arg Gly Pro Arg Pro Thr Glu Asp Gln Ile Ser Gln Leu Pro Lys Asn
50 55 60

Val Phe Phe Leu Leu Asp Asn Ser Ile Asp Met Ser Ile Glu Thr Gly
65 70 75 80

Glu Glu Asn Arg His Phe Leu Ser Glu Phe Phe Lys Leu Leu Lys Lys
85 90 95

Tyr Glu Gly Ile Asn Val Ser Leu Ile Arg Tyr Asn Ser Glu Glu Pro
100 105 110

Leu Gly Ser Thr Lys Ala Leu Thr Asn Gly Glu Leu Lys Lys Leu Ser
115 120 125

Asp Asn Ile Pro Thr Lys Met Pro Phe Asp Ile Gly Val Val Pro Thr
130 135 140

Gly Ile Gly Ala Ala Leu Lys Gln Ile Lys Thr Leu Tyr Pro Asp His
145 150 155 160

Glu Lys Phe Leu Val Gly Asn Thr Ile Thr Glu Leu Asp Tyr Ser Lys
165 170 175

Ala Leu Gly Lys Asp Ile Val Val Ile Val Phe Thr Thr Gly His Val
180 185 190

Ile Asp Pro Tyr Leu Ala Tyr Asp Glu Ala Phe Asp Ala Arg Arg Asn
195 200 205

Gly Val Arg Phe Tyr Val Ile Asn Arg Gly Gly Lys Ala Lys Asn Tyr
210 215 220

Trp Thr Gln Leu Leu Gly Cys His Tyr Asn Thr Cys Leu Ser Tyr Ile
225 230 235 240

Arg Ala Lys Ile Thr Arg Pro Ser Leu Tyr Leu Asp Val Leu Val Asn
245 250 255

Arg Ile Val Ser Lys Arg Ala Lys Asp Ala Val Cys Leu Glu Val Trp
260 265 270

Thr Asp Tyr Lys Pro Asn Thr Glu Lys Ser Asp Val Arg Ile Met Thr
275 280 285

Ser Thr Leu Lys Leu Tyr Lys Thr Leu Leu Thr Gly Ser Phe Ala Glu
290 295 300

Xaa Asn Ile Lys Gly Leu Thr Cys Asp Glu Gln Leu Lys Asp Met Gln
305 310 315 320

Lys Arg Gln Ile Phe Cys Tyr Ser Asn Lys Cys Ala Pro Thr Ile Tyr
325 330 335

Ser Arg Ser Tyr Val Asp Leu Ala Ile Gln Arg Leu Asn Ala Lys Asp
340 345 350

Phe Lys Glu Val Leu Asp Glu Ser Ser Tyr Arg Ser Arg Ser Leu Gln
355 360 365

Ser Val Glu Lys His Asn Glu Gln Gln Thr Gly Ser Gln Glu Thr Leu
370 375 380

Ser Gly Ser Ala Arg Val Glu Thr Ser Leu Glu Ser Ser Val Pro Ser
385 390 395 400

Ser Tyr Val Ala Glu Leu Gly Glu Ser Asp Thr Glu Thr Tyr Lys Gln
405 410 415

Leu Glu Tyr Ile Asp Lys Asn Gly Val Thr Val Phe Asn Asp Glu Pro
420 425 430

Thr Val Val Val Asp Thr Pro Glu Tyr Val Gln Lys Val His Glu Arg

435 440 445

Glu Met Gln Phe Asp Glu Glu Ser Thr His Leu Pro Asn Ser Gly Asn
450 455 460

His His Pro Pro His His Arg Lys Gly Ala Asn Gly Ser Gly Lys Lys
465 470 475 480

Thr Thr Ile Val Val Gly Ile Ile Cys Leu Val Val Ile Cys Ala Val
485 490 495

Ile Ala Gly Ala Tyr Leu Ser Leu Ser Gln Gln Glu Ser Val Glu Leu
500 505 510

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